



RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 09/466,778A
Source: 1609
Date Processed by STIC: 8/14/2003

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

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U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

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Revised 04/24/2003



1600

RAW SEQUENCE LISTING

DATE: 08/14/2003

PATENT APPLICATION: US/09/466,778A

TIME: 15:07:38

Input Set : A:\PF487 subst. SL Aug2003.txt

Output Set: N:\CRF4\08142003\I466778A.raw

3 <110> APPLICANT: Hastings, et al.
5 <120> TITLE OF INVENTION: Novel Hyaluronan-Binding Proteins and Encoding Genes
7 <130> FILE REFERENCE: PF487
9 <140> CURRENT APPLICATION NUMBER: 09/466,778A
10 <141> CURRENT FILING DATE: 1999-12-20
12 <150> PRIOR APPLICATION NUMBER: 60/113,871
13 <151> PRIOR FILING DATE: 1998-12-23
15 <160> NUMBER OF SEQ ID NOS: 37
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 6761
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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29 <221> NAME/KEY: misc_feature
30 <222> LOCATION: (6342)
31 <223> OTHER INFORMATION: n equals a, t, g or c
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39 <221> NAME/KEY: misc_feature
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49 <221> NAME/KEY: misc_feature
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56 <223> OTHER INFORMATION: n equals a, t, g or c
58 <220> FEATURE:
59 <221> NAME/KEY: misc_feature
60 <222> LOCATION: (6724)

Does Not Comply
Corrected Diskette Needed

pg 2, 6-7

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Input Set : A:\PF487 subst. SL Aug2003.txt

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83 ggccacgcag acaggccggg tgttctcgca gctgaggggc gccgtggcc atg atg gac 178
84 Met Met Asp
85 1
87 cag ggc tgc cgg gaa atc ctt acc aca gcg ggc cct ttc acc gtg ctg 226
88 Gln Gly Cys Arg Glu Ile Leu Thr Thr Ala Gly Pro Phe Thr Val Leu
89 5 10 15
91 gtg cca tcc gtc tcc tcc ttc tcc tcc agg acc atg aat gca tcc ctt 274
92 Val Pro Ser Val Ser Ser Phe Ser Ser Arg Thr Met Asn Ala Ser Leu
93 20 25 30 35
95 gcc cag cag ctc tgt aga cag cac atc atc gca ggg cag cac atc ctg 322
96 Ala Gln Gln Leu Cys Arg Gln His Ile Ile Ala Gly Gln His Ile Leu
97 40 45 50
99 gag gac aca agg acc caa caa aca cga agg tgg tgg acg ctg gcc ggg 370
100 Glu Asp Thr Arg Thr Gln Gln Thr Arg Arg Trp Trp Thr Leu Ala Gly
101 55 60 65
103 cag gag atc acc gtc acc ttt aac caa ttc acg aaa tac tcc tac aag 418
104 Gln Glu Ile Thr Val Thr Phe Asn Gln Phe Thr Lys Tyr Ser Tyr Lys
105 70 75 80
107 tac aaa gac cag ccc cag cag acg ttc aac atc tac aag gcc aac aac 466
108 Tyr Lys Asp Gln Pro Gln Gln Thr Phe Asn Ile Tyr Lys Ala Asn Asn
109 85 90 95
111 ata gca gct aat ggc gtc ttc cac gtg gtc act ggc ctg cgg tgg cag 514
112 Ile Ala Ala Asn Gly Val Phe His Val Val Thr Gly Leu Arg Trp Gln
113 100 105 110 115
115 gcc ccc tct ggg acc cct ggg gat ccc aag aga act atc gga cag atc 562
116 Ala Pro Ser Gly Thr Pro Gly Asp Pro Lys Arg Thr Ile Gly Gln Ile
117 120 125 130
119 ctc gcc tct acc gag gcc ttc agc cgc ttt gaa acc atc ctg gag aac 610
120 Leu Ala Ser Thr Glu Ala Phe Ser Arg Phe Glu Thr Ile Leu Glu Asn
121 135 140 145
123 tgt ggg ctg ccc tcc atc ctg gac gga cct ggg ccc ttc aca gtc ttt 658
124 Cys Gly Leu Pro Ser Ile Leu Asp Gly Pro Gly Pro Phe Thr Val Phe
125 150 155 160

*what about "n" at location
6749?
(see p.6)*

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Input Set : A:\PF487 subst. SL Aug2003.txt

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127	gcc	cca	agc	aat	gag	gct	gtg	gac	agc	ttg	cgt	gac	ggc	cgc	ctg	atc	706
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129	165						170					175					
131	tac	ctc	ttc	aca	gcg	ggt	ctc	tct	aaa	ctg	cag	gag	ttg	gtg	cgg	tac	754
132	Tyr	Leu	Phe	Thr	Ala	Gly	Leu	Ser	Lys	Leu	Gln	Glu	Leu	Val	Arg	Tyr	
133	180					185					190					195	
135	cac	atc	tac	aac	cac	ggc	cag	ctg	acc	ggt	gag	aag	ctc	atc	tcc	aag	802
136	His	Ile	Tyr	Asn	His	Gly	Gln	Leu	Thr	Val	Glu	Lys	Leu	Ile	Ser	Lys	
137	200									205					210		
139	ggt	cgg	atc	ctc	acc	atg	gcg	aac	cag	gtc	ctg	gct	gtg	aac	att	tct	850
140	Gly	Arg	Ile	Leu	Thr	Met	Ala	Asn	Gln	Val	Leu	Ala	Val	Asn	Ile	Ser	
141	215								220					225			
143	gag	gag	ggg	cgc	atc	ctg	ctg	gga	ccc	gag	ggg	gtc	ccg	ctg	cag	agg	898
144	Glu	Glu	Gly	Arg	Ile	Leu	Leu	Gly	Pro	Glu	Gly	Val	Pro	Leu	Gln	Arg	
145	230							235					240				
147	gta	gac	gtg	atg	gcc	gcc	aat	ggc	gtg	atc	cac	atg	ctg	gac	ggc	atc	946
148	Val	Asp	Val	Met	Ala	Ala	Asn	Gly	Val	Ile	His	Met	Leu	Asp	Gly	Ile	
149	245						250					255					
151	ctg	ctg	ccc	ccg	acc	atc	ctg	ccc	atc	ctg	ccc	aag	cac	tgc	agc	gag	994
152	Leu	Leu	Pro	Pro	Thr	Ile	Leu	Pro	Ile	Leu	Pro	Lys	His	Cys	Ser	Glu	
153	260					265					270				275		
155	gag	cag	cac	aag	att	gtg	gcg	ggc	tcc	tgt	gtg	gac	tgc	caa	gcc	ctg	1042
156	Glu	Gln	His	Lys	Ile	Val	Ala	Gly	Ser	Cys	Val	Asp	Cys	Gln	Ala	Leu	
157	280								285					290			
159	aac	acc	agc	acg	tgt	ccc	ccc	aac	agt	gtg	aag	ctg	gac	atc	ttc	ccc	1090
160	Asn	Thr	Ser	Thr	Cys	Pro	Pro	Asn	Ser	Val	Lys	Leu	Asp	Ile	Phe	Pro	
161	295								300					305			
163	aag	gag	tgt	gtc	tac	atc	cat	gac	cca	acg	ggg	ctc	aat	gtg	cta	aag	1138
164	Lys	Glu	Cys	Val	Tyr	Ile	His	Asp	Pro	Thr	Gly	Leu	Asn	Val	Leu	Lys	
165	310							315					320				
167	aag	ggc	tgt	gcc	agc	tac	tgc	aac	caa	acc	atc	atg	gaa	caa	ggc	tgc	1186
168	Lys	Gly	Cys	Ala	Ser	Tyr	Cys	Asn	Gln	Thr	Ile	Met	Glu	Gln	Gly	Cys	
169	325							330				335					
171	tgc	aaa	ggt	ttt	ttc	ggg	cct	gac	tgc	acg	cag	tgt	cct	ggg	ggc	ttc	1234
172	Cys	Lys	Gly	Phe	Phe	Gly	Pro	Asp	Cys	Thr	Gln	Cys	Pro	Gly	Gly	Phe	
173	340					345					350				355		
175	tcc	aac	ccc	tgc	tat	ggc	aaa	ggc	aat	tgc	agt	gat	ggg	atc	cag	ggc	1282
176	Ser	Asn	Pro	Cys	Tyr	Gly	Lys	Gly	Asn	Cys	Ser	Asp	Gly	Ile	Gln	Gly	
177	360								365					370			
179	aat	ggg	gcc	tgc	ctc	tgc	ttc	cca	gac	tac	aag	ggc	atc	gcc	tgc	cac	1330
180	Asn	Gly	Ala	Cys	Leu	Cys	Phe	Pro	Asp	Tyr	Lys	Gly	Ile	Ala	Cys	His	
181	375								380					385			
183	atc	tgc	tcg	aac	cca	aac	aag	cat	gga	gag	caa	tgc	cag	gaa	gac	tgc	1378
184	Ile	Cys	Ser	Asn	Pro	Asn	Lys	His	Gly	Glu	Gln	Cys	Gln	Glu	Asp	Cys	
185	390							395					400				
187	ggc	tgt	gtc	cat	ggt	ctc	tgc	gac	aac	cgc	cca	ggc	agt	ggg	ggg	gtg	1426
188	Gly	Cys	Val	His	Gly	Leu	Cys	Asp	Asn	Arg	Pro	Gly	Ser	Gly	Gly	Val	
189	405						410						415				
191	tgc	cag	cag	ggc	acg	tgt	gcc	cct	ggc	ttc	agt	ggc	cgg	ttc	tgc	aac	1474

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192	Cys	Gln	Gln	Gly	Thr	Cys	Ala	Pro	Gly	Phe	Ser	Gly	Arg	Phe	Cys	Asn	
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195	gag	tcc	atg	ggg	gac	tgt	ggg	ccc	aca	ggg	ctg	gcc	cag	cac	tgc	cac	1522
196	Glu	Ser	Met	Gly	Asp	Cys	Gly	Pro	Thr	Gly	Leu	Ala	Gln	His	Cys	His	
197					440					445						450	
199	ctg	cat	gcc	cgc	tgt	gtt	agc	cag	gag	ggt	gtt	gcc	aga	tgt	cgc	tgt	1570
200	Leu	His	Ala	Arg	Cys	Val	Ser	Gln	Glu	Gly	Val	Ala	Arg	Cys	Arg	Cys	
201					455					460						465	
203	ctt	gat	ggc	ttt	gag	ggt	gat	ggc	ttc	tgc	aca	cct	agc	aac	ccc		1618
204	Leu	Asp	Gly	Phe	Glu	Gly	Asp	Gly	Phe	Ser	Cys	Thr	Pro	Ser	Asn	Pro	
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207	tgc	tcc	cac	ccg	gac	cgt	gga	ggc	tgc	tca	gag	aat	gct	gag	tgt	gtc	1666
208	Cys	Ser	His	Pro	Asp	Arg	Gly	Gly	Cys	Ser	Glu	Asn	Ala	Glu	Cys	Val	
209			485					490					495				
211	oct	ggg	tcc	ctg	ggc	acc	cac	cac	tgc	aca	tgc	cac	aaa	ggc	tgg	agt	1714
212	Pro	Gly	Ser	Leu	Gly	Thr	His	His	Cys	Thr	Cys	His	Lys	Gly	Trp	Ser	
213	500					505					510					515	
215	ggg	gat	ggc	cgc	gtc	tgt	gtg	gct	att	gac	gag	tgt	gag	ctg	gac	gtg	1762
216	Gly	Asp	Gly	Arg	Val	Cys	Val	Ala	Ile	Asp	Glu	Cys	Glu	Leu	Asp	Val	
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220	Arg	Gly	Gly	Cys	His	Thr	Asp	Ala	Leu	Cys	Ser	Tyr	Val	Gly	Pro	Gly	
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224	Gln	Ser	Arg	Cys	Thr	Cys	Lys	Leu	Gly	Phe	Ala	Gly	Asp	Gly	Tyr	Gln	
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232	Leu	Glu	Leu	Glu	Ala	Asn	Ala	His	Phe	Ser	Ile	Phe	Tyr	Gln	Trp	Leu	
233	580					585							590			595	
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236	Lys	Ser	Ala	Gly	Ile	Thr	Leu	Pro	Ala	Asp	Arg	Arg	Val	Thr	Ala	Leu	
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239	gtg	ccc	tcc	gag	gct	gca	gtc	cgt	cag	ctg	agc	ccc	gag	gac	cga	gct	2050
240	Val	Pro	Ser	Glu	Ala	Ala	Val	Arg	Gln	Leu	Ser	Pro	Glu	Asp	Arg	Ala	
241					615				620							625	
243	ttc	tgg	ctg	cag	cca	agg	acg	ctg	ccg	aac	ctg	gtc	agg	gcc	cat	ttt	2098
244	Phe	Trp	Leu	Gln	Pro	Arg	Thr	Leu	Pro	Asn	Leu	Val	Arg	Ala	His	Phe	
245			630					635					640				
247	ctc	cag	ggt	gcc	ctc	ttc	gag	gag	gag	ctg	gcc	cgg	ctg	ggt	ggg	cag	2146
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253	660					665					670					675	
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261          695          700          705
263 ccc cga ggg gat gtg ccc ggt ggg cag ggg ttg ctg cag cag ctg gac 2338
264 Pro Arg Gly Asp Val Pro Gly Gly Gln Gly Leu Leu Gln Gln Leu Asp
265          710          715          720
267 ttg gtg cct gcc ttc agc ctc ttc cgg gaa ttg ctg cag cac cat ggg 2386
268 Leu Val Pro Ala Phe Ser Leu Phe Arg Glu Leu Leu Gln His His Gly
269          725          730          735
271 ttg gtg ccc cag att gag gct gcc act gcc tac acc atc ttt gtg ccc 2434
272 Leu Val Pro Gln Ile Glu Ala Ala Thr Ala Tyr Thr Ile Phe Val Pro
273 740          745          750          755
275 acc aac cgc tcc ctg gag gcc cag ggc aac agc agt cac ctg gac gca 2482
276 Thr Asn Arg Ser Leu Glu Ala Gln Gly Asn Ser Ser His Leu Asp Ala
277          760          765          770
279 gac aca gtg cgg cac cat gtg gtc ctg ggg gag gcc ctc tcc atg gaa 2530
280 Asp Thr Val Arg His His Val Val Leu Gly Glu Ala Leu Ser Met Glu
281          775          780          785
283 acc ctg cgg aag ggt gga cac cgc aac tcc ctc ctg ggc cct gcc cac 2578
284 Thr Leu Arg Lys Gly Gly His Arg Asn Ser Leu Leu Gly Pro Ala His
285          790          795          800
287 tgg atc gtc ttc tac aac cac agt ggc cag cct gag gtg aac cat gtg 2626
288 Trp Ile Val Phe Tyr Asn His Ser Gly Gln Pro Glu Val Asn His Val
289          805          810          815
291 cca ctg gaa ggc ccc atg ctg gag gcc cct ggc cgc tcg ctg att ggt 2674
292 Pro Leu Glu Gly Pro Met Leu Glu Ala Pro Gly Arg Ser Leu Ile Gly
293 820          825          830          835
295 ctg tcg ggg gtc ctg acg gtg ggc tca agt cgc tgc ctg cat agc cac 2722
296 Leu Ser Gly Val Leu Thr Val Gly Ser Ser Arg Cys Leu His Ser His
297          840          845          850
299 gct gag gcc ctg cgg gag aaa tgt gta aac tgc acc agg aga ttc cgc 2770
300 Ala Glu Ala Leu Arg Glu Lys Cys Val Asn Cys Thr Arg Arg Phe Arg
301          855          860          865
303 tgc act cag ggc ttc cag ctg cag gac aca ccc agg aag agc tgt gtc 2818
304 Cys Thr Gln Gly Phe Gln Leu Gln Asp Thr Pro Arg Lys Ser Cys Val
305          870          875          880
307 tac cga tct ggc ttc tcc ttc tcc cgg ggc tgc tct tac aca tgt gcc 2866
308 Tyr Arg Ser Gly Phe Ser Phe Ser Arg Gly Cys Ser Tyr Thr Cys Ala
309          885          890          895
311 aag aag atc cag gtg ccg gac tgc tgc cct ggt ttc ttt ggc acg ctg 2914
312 Lys Lys Ile Gln Val Pro Asp Cys Cys Pro Gly Phe Phe Gly Thr Leu
313 900          905          910          915
315 tgt gag cca tgc cca ggg ggt cta ggg ggg gtg tgc tca ggc cat ggg 2962
316 Cys Glu Pro Cys Pro Gly Gly Leu Gly Gly Val Cys Ser Gly His Gly
317          920          925          930
319 cag tgc cag gac agg ttc ctg ggc agc ggg gag tgc cac tgc cac gag 3010
320 Gln Cys Gln Asp Arg Phe Leu Gly Ser Gly Glu Cys His Cys His Glu
321          935          940          945

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09/466,778A 6

gaagcatgca cagggaggag accantttta ttgcttgtct gggtaggatgg ggcaggaggg 6723
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↓
location 6749

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/466,778A

DATE: 08/14/2003
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Input Set : A:\PF487 subst. SL Aug2003.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:2; Xaa Pos. 2058,2109,2120,2122,2123
Seq#:4; N Pos. 1103,1257,1290,1296,1298,1449,1485,1509,1510,1511,1514
Seq#:4; Xaa Pos. 358,409,420,422,423
Seq#:5; Xaa Pos. 358,409,420,422,423
Seq#:7; N Pos. 36,51,248,508,521,564,933,945,951,958
Seq#:7; Xaa Pos. 44,131,135,149,265,272,276,278,281
Seq#:8; Xaa Pos. 44,131,135,149,265,272,276,278,281
Seq#:10; N Pos. 478,479,668,849,1138,1149,1157,1169,1172,1251
Seq#:10; Xaa Pos. 94,157,303,314,320,324,325,351
Seq#:11; Xaa Pos. 94,157,303,314,320,324,325,351
Seq#:18; N Pos. 40
Seq#:20; N Pos. 21
Seq#:26; N Pos. 40
Seq#:28; N Pos. 21
Seq#:34; N Pos. 40
Seq#:36; N Pos. 21